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<211> 319  
<212> PRT  
<213> Homo sapiens

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<222> 1-17  
<223> Signal Peptide

<220>  
<221> misc\_feature

<222> 36-47, 108-113, 166-171,198-203, 207-212  
 <223> N-myristoylation Sites.

<220>  
 <221> misc\_feature  
 <222> 39-42  
 <223> Glycosaminoglycan Attachment Site.

<220>  
 <221> TRANSMEM  
 <222> 136-152  
 <223> Transmembrane Domain

<220>  
 <221> misc\_feature  
 <222> 161-163, 187-190 and 253-256  
 <223> N-glycosylation Sites.

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 Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala  
 35 40 45  
 Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys  
 50 55 60  
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 65 70 75  
 Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val  
 80 85 90  
 Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly  
 95 100 105  
 Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala  
 110 115 120  
 Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu  
 125 130 135  
 Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro  
 140 145 150  
 Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val  
 155 160 165  
 Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys  
 170 175 180  
 Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys  
 185 190 195

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys  
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 Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala  
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 Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu  
 230 235 240  
 Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser  
 245 250 255  
 Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His  
 260 265 270  
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 Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala  
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 <211> 699  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> TRANSMEM  
 <222> 21-40 and 84-105  
 <223> Transmembrane Domain (type II)

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 35 40 45  
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
 50 55 60  
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp  
 65 70 75  
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
 80 85 90  
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala  
 95 100 105

Asp	His	Trp	Lys	Ala 110	Leu	Ala	Phe	Arg	Leu 115	Glu	Glu	Glu	Gln	Lys 120
Met	Arg	Pro	Glu	Ile 125	Ala	Gly	Leu	Lys	Pro 130	Ala	Asn	Pro	Pro	Val 135
Leu	Pro	Ala	Pro	Gln 140	Lys	Ala	Asp	Thr	Asp 145	Pro	Glu	Asn	Leu	Pro 150
Glu	Ile	Ser	Ser	Gln 155	Lys	Thr	Gln	Arg	His 160	Ile	Gln	Arg	Gly	Pro 165
Pro	His	Leu	Gln	Ile 170	Arg	Pro	Pro	Ser	Gln 175	Asp	Leu	Lys	Asp	Gly 180
Thr	Gln	Glu	Glu	Ala 185	Thr	Lys	Arg	Gln	Glu 190	Ala	Pro	Val	Asp	Pro 195
Arg	Pro	Glu	Gly	Asp 200	Pro	Gln	Arg	Thr	Val 205	Ile	Ser	Trp	Arg	Gly 210
Ala	Val	Ile	Glu	Pro 215	Glu	Gln	Gly	Thr	Glu 220	Leu	Pro	Ser	Arg	Arg 225
Ala	Glu	Val	Pro	Thr 230	Lys	Pro	Pro	Leu	Pro 235	Pro	Ala	Arg	Thr	Gln 240
Gly	Thr	Pro	Val	His 245	Leu	Asn	Tyr	Arg	Gln 250	Lys	Gly	Val	Ile	Asp 255
Val	Phe	Leu	His	Ala 260	Trp	Lys	Gly	Tyr	Arg 265	Lys	Phe	Ala	Trp	Gly 270
His	Asp	Glu	Leu	Lys 275	Pro	Val	Ser	Arg	Ser 280	Phe	Ser	Glu	Trp	Phe 285
Gly	Leu	Gly	Leu	Thr 290	Leu	Ile	Asp	Ala	Leu 295	Asp	Thr	Met	Trp	Ile 300
Leu	Gly	Leu	Arg	Lys 305	Glu	Phe	Glu	Glu	Ala 310	Arg	Lys	Trp	Val	Ser 315
Lys	Lys	Leu	His	Phe 320	Glu	Lys	Asp	Val	Asp 325	Val	Asn	Leu	Phe	Glu 330
Ser	Thr	Ile	Arg	Ile 335	Leu	Gly	Gly	Leu	Leu 340	Ser	Ala	Tyr	His	Leu 345
Ser	Gly	Asp	Ser	Leu 350	Phe	Leu	Arg	Lys	Ala 355	Glu	Asp	Phe	Gly	Asn 360
Arg	Leu	Met	Pro	Ala 365	Phe	Arg	Thr	Pro	Ser 370	Lys	Ile	Pro	Tyr	Ser 375
Asp	Val	Asn	Ile	Gly 380	Thr	Gly	Val	Ala	His 385	Pro	Pro	Arg	Trp	Thr 390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe

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Val	Glu	Lys	Val	Thr 425	Gln	His	Ile	His	Gly 430	Leu	Ser	Gly	Lys	Lys 435				
Asp	Gly	Leu	Val	Pro 440	Met	Phe	Ile	Asn	Thr 445	His	Ser	Gly	Leu	Phe 450				
Thr	His	Leu	Gly	Val 455	Phe	Thr	Leu	Gly	Ala 460	Arg	Ala	Asp	Ser	Tyr 465				
Tyr	Glu	Tyr	Leu	Leu 470	Lys	Gln	Trp	Ile	Gln 475	Gly	Gly	Lys	Gln	Glu 480				
Thr	Gln	Leu	Leu	Glu 485	Asp	Tyr	Val	Glu	Ala 490	Ile	Glu	Gly	Val	Arg 495				
Thr	His	Leu	Leu	Arg 500	His	Ser	Glu	Pro	Ser 505	Lys	Leu	Thr	Phe	Val 510				
Gly	Glu	Leu	Ala	His 515	Gly	Arg	Phe	Ser	Ala 520	Lys	Met	Asp	His	Leu 525				
Val	Cys	Phe	Leu	Pro 530	Gly	Thr	Leu	Ala	Leu 535	Gly	Val	Tyr	His	Gly 540				
Leu	Pro	Ala	Ser	His 545	Met	Glu	Leu	Ala	Gln 550	Glu	Leu	Met	Glu	Thr 555				
Cys	Tyr	Gln	Met	Asn 560	Arg	Gln	Met	Glu	Thr 565	Gly	Leu	Ser	Pro	Glu 570				
Ile	Val	His	Phe	Asn 575	Leu	Tyr	Pro	Gln	Pro 580	Gly	Arg	Arg	Asp	Val 585				
Glu	Val	Lys	Pro	Ala 590	Asp	Arg	His	Asn	Leu 595	Leu	Arg	Pro	Glu	Thr 600				
Val	Glu	Ser	Leu	Phe 605	Tyr	Leu	Tyr	Arg	Val 610	Thr	Gly	Asp	Arg	Lys 615				
Tyr	Gln	Asp	Trp	Gly 620	Trp	Glu	Ile	Leu	Gln 625	Ser	Phe	Ser	Arg	Phe 630				
Thr	Arg	Val	Pro	Ser 635	Gly	Gly	Tyr	Ser	Ser 640	Ile	Asn	Asn	Val	Gln 645				
Asp	Pro	Gln	Lys	Pro 650	Glu	Pro	Arg	Asp	Lys 655	Met	Glu	Ser	Phe	Phe 660				
Leu	Gly	Glu	Thr	Leu 665	Lys	Tyr	Leu	Phe	Leu 670	Leu	Phe	Ser	Asp	Asp 675				
Pro	Asn	Leu	Leu	Ser 680	Leu	Asp	Ala	Tyr	Val 685	Phe	Asn	Thr	Glu	Ala 690				

His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
cgccagaagg gcgtgattga cgtc 24

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 14  
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<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 15  
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<210> 16  
<211> 1524  
<212> DNA  
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<400> 16  
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gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

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<210> 17
<211> 327
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<221> sig\_peptide  
<222> 1-42  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 19-25, 65-71, 247-253, 285-291, 303-310  
<223> N-myristoylation site.

<220>  
<221> misc\_feature  
<222> 27-31  
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
<221> TRANSMEM  
<222> 29-49  
<223> Transmembrane domain (type II).

<220>  
<221> misc\_feature  
<222> 154-158  
<223> N-glycosylation site.

<220>  
<221> misc\_feature  
<222> 226-233  
<223> Tyrosine kinase phosphorylation site.

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35 40 45  
Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala  
50 55 60  
Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys  
65 70 75  
Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp  
80 85 90  
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe  
95 100 105  
Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser  
110 115 120  
Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp  
125 130 135  
His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

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Glu Ser Ser Asn	Ser Thr Asp Tyr Ile	Ala Met His Asp Val	Asp		
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Leu Leu Pro Leu	Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu	Ala		
	170		175		180
Gly Pro Phe His	Val Ala Ser Pro Glu	Leu His Pro Leu Tyr	His		
	185		190		195
Tyr Lys Thr Tyr	Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln	His		
	200		205		210
Tyr Arg Leu Cys	Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp	Gly		
	215		220		225
Arg Glu Asp Asp	Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly	Leu		
	230		235		240
Gln Leu Phe Arg	Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr	Phe		
	245		250		255
Arg His Leu His	Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys	Arg		
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Ile Ala Ala Gln	Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu	Gly		
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Gly Leu Asn Thr	Val Lys Tyr His Val	Ala Ser Arg Thr Ala	Leu		
	290		295		300
Ser Val Gly Gly	Ala Pro Cys Thr Val	Leu Asn Ile Met Leu	Asp		
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Cys Asp Lys Thr	Ala Thr Pro Trp Cys	Thr Phe Ser			
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 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-23  
 <223> Synthetic construct.

<400> 18  
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<210> 19  
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 <212> DNA  
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<220>  
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<222> 1-24  
 <223> Synthetic construct

<400> 19  
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<210> 20  
 <211> 46  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-46  
 <223> Synthetic construct.

<400> 20  
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<210> 21  
 <211> 494  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
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 gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150  
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<210> 22  
 <211> 73  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> 1-15  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 3-18



<223> Growth factor and cytokines receptors family.

<400> 22

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Ala	Thr	Asp	Ala	Pro	Ile	Arg	Asp	Trp	Ala	Phe	Phe	Pro	Ser
			35					40					45
Phe	Leu	Cys	Leu	Leu	Pro	His	Arg	Pro	Ala	Met	Thr	Cys	Gln
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Ala	Gln	Pro	Arg	Gly	Glu	Gly	Glu	Lys	Val	Gly	Asp	Gly	
			65					70					

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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<210> 24  
 <211> 616  
 <212> PRT  
 <213> Homo sapiens  
  
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 <221> sig\_peptide  
 <222> 1-33  
 <223> Signal peptide.

<220>  
 <221> TRANSMEM  
 <222> 13-40  
 <223> Transmembrane domain (type II).

<400> 24  
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 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly  
 20 25 30  
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His  
 35 40 45  
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
 50 55 60  
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
 65 70 75  
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
 80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser	95	100	105
Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile	110	115	120
Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp	125	130	135
Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg	140	145	150
Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe	155	160	165
Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg	170	175	180
Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile	185	190	195
Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg	200	205	210
Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val	215	220	225
Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu	230	235	240
Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe	245	250	255
Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp	260	265	270
Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu	275	280	285
Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His	290	295	300
Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln	305	310	315
Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg	320	325	330
Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser	335	340	345
Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp	350	355	360
Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln	365	370	375
Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro			

380									385					390	
Gln	Asp	Glu	Arg	Lys 395	Ala	Trp	Arg	Arg	Cys 400	Asp	Arg	Gly	Gly	Phe 405	
Trp	Ala	Asp	Asp	Asp 410	Tyr	Ser	Arg	Cys	Gln 415	Tyr	Ala	Asn	Asp	Val 420	
Thr	Arg	Val	Leu	Tyr 425	Met	Phe	Asn	Gln	Met 430	Pro	Leu	Asn	Leu	Thr 435	
Asn	Ala	Val	Ala	Thr 440	Ala	Arg	Gln	Leu	Leu 445	Ala	Tyr	Thr	Val	Glu 450	
Ala	Ala	Asn	Phe	Ser 455	Asp	Lys	Met	Asp	Val 460	Ile	Phe	Val	Ala	Glu 465	
Met	Ile	Glu	Lys	Phe 470	Gly	Arg	Phe	Thr	Lys 475	Glu	Glu	Lys	Ser	Lys 480	
Glu	Leu	Gly	Asp	Val 485	Met	Val	Asp	Ile	Ala 490	Ser	Asn	Ile	Met	Leu 495	
Ala	Asp	Glu	Arg	Val 500	Leu	Trp	Leu	Ala	Gln 505	Arg	Glu	Ala	Lys	Ala 510	
Cys	Ser	Arg	Ile	Val 515	Gln	Cys	Leu	Gln	Arg 520	Ile	Ala	Thr	Tyr	Arg 525	
Leu	Ala	Gly	Gly	Ala 530	His	Val	Tyr	Ser	Thr 535	Tyr	Ser	Pro	Asn	Ile 540	
Ala	Leu	Glu	Ala	Tyr 545	Val	Ile	Lys	Ser	Thr 550	Gly	Phe	Thr	Gly	Met 555	
Thr	Cys	Thr	Val	Phe 560	Gln	Lys	Val	Ala	Ala 565	Ser	Asp	Arg	Thr	Gly 570	
Leu	Ser	Asp	Tyr	Gly 575	Arg	Arg	Asp	Pro	Glu 580	Gly	Asn	Leu	Asp	Lys 585	
Gln	Leu	Ser	Phe	Lys 590	Cys	Asn	Val	Ser	Asn 595	Thr	Phe	Ser	Ser	Leu 600	
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Ser

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<210> 25
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
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<223> Synthetic construct

<400> 25

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<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accagggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcggg 150

aaaaagaaaa cattcgtctt ttgggagaac agattatctt gactgagcaa 200

cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaaatc 250

atgacttgaa tgtgaaatat ctgttggaac gacaacacga gtttgtgtgt 300

gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350

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<210> 29  
<211> 81  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-21  
<223> Signal peptide.

<400> 29  
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20 25 30  
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35 40 45  
Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
50 55 60  
Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala  
65 70 75  
Lys Gly Ser Gln Lys Ser  
80

<210> 30  
<211> 2128  
<212> DNA  
<213> Homo sapiens

<400> 30  
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caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggcccccca 200  
tgatcgtagg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250  
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<210> 31  
<211> 322  
<212> PRT  
<213> Homo sapiens

<400> 31  
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35 40 45  
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp  
50 55 60  
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
65 70 75  
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
80 85 90  
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
95 100 105  
Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr  
110 115 120  
Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp  
125 130 135  
His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala  
140 145 150  
Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile  
155 160 165  
Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu  
170 175 180  
Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn  
185 190 195  
Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr  
200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu  
215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu  
230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu  
245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln  
260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr  
275 280 285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr  
290 295 300

Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala  
305 310 315

His Leu Val Phe Val Lys Val  
320

<210> 32  
<211> 3680  
<212> DNA  
<213> Homo sapiens

<400> 32  
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taatataaaaa atcttttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
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Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180
Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
				185					190					195
His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240



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 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 37  
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<210> 38  
 <211> 39  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-39  
 <223> Synthetic construct.

<400> 38  
 ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 39  
 ctgctgcaaa gcgagcctct tg 22

<210> 40  
 <211> 2084  
 <212> DNA  
 <213> Homo sapiens

<400> 40  
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 ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150  
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ttgggtgcct taaaaactca atgagaatca tgggt 2084

<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
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20 25 30  
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105  
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
110 115 120  
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
125 130 135  
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
140 145 150  
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
155 160 165  
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
170 175 180  
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu  
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn  
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe  
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu  
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser  
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu  
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser  
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu  
305 310 315

Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu  
320 325 330

Arg Thr Ser Val

<210> 42  
<211> 1594  
<212> DNA  
<213> Homo sapiens

<400> 42  
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tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250  
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tacaagtact tcatgcccga gagcaccatt taccgtggag agatgtgctt 350  
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tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450  
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ggaactgcta tctgatgccc ctcaatactt ctattgttat gcctccaaaa 600  
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gaaaaaaaa aaaactacta accactgcaa gctcttgta aatttttagtt 1050  
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ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450  
aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500  
tgtgtagggt ctgaatgctg taaggagttt aggttgatg aattctacaa 1550  
ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43  
<211> 263  
<212> PRT  
<213> Homo sapiens

<400> 43  
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20 25 30  
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu  
35 40 45  
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50										55					60				
Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr					
				65					70					75					
Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys					
				80					85					90					
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu					
				95					100					105					
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp					
				110					115					120					
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp					
				125					130					135					
Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr					
				140					145					150					
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu					
				155					160					165					
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe					
				170					175					180					
Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val					
				185					190					195					
Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn					
				200					205					210					
Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe					
				215					220					225					
Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala					
				230					235					240					
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile					
				245					250					255					
Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu												
				260															

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45



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ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850  
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900  
attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950  
aaaaaaaaa aaaaaaaga 1969

<210> 50  
<211> 283  
<212> PRT  
<213> Homo sapiens

<400> 50  
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20 25 30  
Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
35 40 45  
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
50 55 60  
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
65 70 75  
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe  
80 85 90  
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala  
95 100 105  
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln  
110 115 120  
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys  
125 130 135  
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe  
140 145 150  
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala  
155 160 165

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr  
170 175 180  
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp  
185 190 195  
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys  
200 205 210  
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro  
215 220 225  
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu  
230 235 240  
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly  
245 250 255  
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro  
260 265 270  
Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val  
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<210> 51  
<211> 1734  
<212> DNA  
<213> Homo sapiens

<400> 51  
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agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200  
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ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700



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ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
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<210> 52
<211> 440
<212> PRT
<213> Homo sapiens
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Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
             20             25             30
Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
             35             40             45
Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly
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				50						55					60
Gly	Ala	Ala	Gly	Ser 65	Lys	Val	Ser	Glu	Ala 70	Leu	Gly	Gln	Gly	Thr 75	
Arg	Glu	Ala	Val	Gly 80	Thr	Gly	Val	Arg	Gln 85	Val	Pro	Gly	Phe	Gly 90	
Ala	Ala	Asp	Ala	Leu 95	Gly	Asn	Arg	Val	Gly 100	Glu	Ala	Ala	His	Ala 105	
Leu	Gly	Asn	Thr	Gly 110	His	Glu	Ile	Gly	Arg 115	Gln	Ala	Glu	Asp	Val 120	
Ile	Arg	His	Gly	Ala 125	Asp	Ala	Val	Arg	Gly 130	Ser	Trp	Gln	Gly	Val 135	
Pro	Gly	His	Ser	Gly 140	Ala	Trp	Glu	Thr	Ser 145	Gly	Gly	His	Gly	Ile 150	
Phe	Gly	Ser	Gln	Gly 155	Gly	Leu	Gly	Gly	Gln 160	Gly	Gln	Gly	Asn	Pro 165	
Gly	Gly	Leu	Gly	Thr 170	Pro	Trp	Val	His	Gly 175	Tyr	Pro	Gly	Asn	Ser 180	
Ala	Gly	Ser	Phe	Gly 185	Met	Asn	Pro	Gln	Gly 190	Ala	Pro	Trp	Gly	Gln 195	
Gly	Gly	Asn	Gly	Gly 200	Pro	Pro	Asn	Phe	Gly 205	Thr	Asn	Thr	Gln	Gly 210	
Ala	Val	Ala	Gln	Pro 215	Gly	Tyr	Gly	Ser	Val 220	Arg	Ala	Ser	Asn	Gln 225	
Asn	Glu	Gly	Cys	Thr 230	Asn	Pro	Pro	Pro	Ser 235	Gly	Ser	Gly	Gly	Gly 240	
Ser	Ser	Asn	Ser	Gly 245	Gly	Gly	Ser	Gly	Ser 250	Gln	Ser	Gly	Ser	Ser 255	
Gly	Ser	Gly	Ser	Asn 260	Gly	Asp	Asn	Asn	Asn 265	Gly	Ser	Ser	Ser	Gly 270	
Gly	Ser	Ser	Ser	Gly 275	Ser	Ser	Ser	Gly	Ser 280	Ser	Ser	Gly	Gly	Ser 285	
Ser	Gly	Gly	Ser	Ser 290	Gly	Gly	Ser	Ser	Gly 295	Asn	Ser	Gly	Gly	Ser 300	
Arg	Gly	Asp	Ser	Gly 305	Ser	Glu	Ser	Ser	Trp 310	Gly	Ser	Ser	Thr	Gly 315	
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Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro  
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Thr Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg  
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Val Val Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln  
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Gly Trp Phe Thr Met Val Ile Ala Val Glu Leu Cys Asp His Val  
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Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	170	175	180	
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Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	200	205	210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	215	220	225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	230	235	240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	245	250	255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	260	265	270	

Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met  
290 295 300

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Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser  
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335 340 345

Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala  
350 355 360

Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala  
365 370 375

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380 385 390

Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln  
395 400 405

Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp  
410 415 420

Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu  
425 430 435

Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg  
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455 460 465

Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser  
470 475 480

Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro  
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Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val  
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Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile  
515 520 525

Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu  
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Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys  
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Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

				560					565					570
Arg	Pro	Lys	Pro	Glu 575	Ile	Met	Ala	Ser	Lys 580	Glu	Gln	Gln	Ile	Gln 585
Arg	Asp	Asp	Pro	Gly 590	Ala	Ser	Pro	Gln	Ser 595	Ser	Ser	Gln	Pro	Asp 600
His	Gly	Arg	Leu	Ser 605	Pro	Pro	Glu	Ala	Pro 610	Asp	Arg	Pro	Thr	Ile 615
Ser	Thr	Ala	Ser	Glu 620	Thr	Ser	Val	Tyr	Val 625	Thr	Trp	Ile	Pro	Arg 630
Gly	Asn	Gly	Gly	Phe 635	Pro	Ile	Gln	Ser	Phe 640	Arg	Val	Glu	Tyr	Lys 645
Lys	Leu	Lys	Lys	Val 650	Gly	Asp	Trp	Ile	Leu 655	Ala	Thr	Ser	Ala	Ile 660
Pro	Pro	Ser	Arg	Leu 665	Ser	Val	Glu	Ile	Thr 670	Gly	Leu	Glu	Lys	Gly 675
Thr	Ser	Tyr	Lys	Phe 680	Arg	Val	Arg	Ala	Leu 685	Asn	Met	Leu	Gly	Glu 690
Ser	Glu	Pro	Ser	Ala 695	Pro	Ser	Arg	Pro	Tyr 700	Val	Val	Ser	Gly	Tyr 705
Ser	Gly	Arg	Val	Tyr 710	Glu	Arg	Pro	Val	Ala 715	Gly	Pro	Tyr	Ile	Thr 720
Phe	Thr	Asp	Ala	Val 725	Asn	Glu	Thr	Thr	Ile 730	Met	Leu	Lys	Trp	Met 735
Tyr	Ile	Pro	Ala	Ser 740	Asn	Asn	Asn	Thr	Pro 745	Ile	His	Gly	Phe	Tyr 750
Ile	Tyr	Tyr	Arg	Pro 755	Thr	Asp	Ser	Asp	Asn 760	Asp	Ser	Asp	Tyr	Lys 765
Lys	Asp	Met	Val	Glu 770	Gly	Asp	Lys	Tyr	Trp 775	His	Ser	Ile	Ser	His 780
Leu	Gln	Pro	Glu	Thr 785	Ser	Tyr	Asp	Ile	Lys 790	Met	Gln	Cys	Phe	Asn 795
Glu	Gly	Gly	Glu	Ser 800	Glu	Phe	Ser	Asn	Val 805	Met	Ile	Cys	Glu	Thr 810
Lys	Ala	Arg	Lys	Ser 815	Ser	Gly	Gln	Pro	Gly 820	Arg	Leu	Pro	Pro	Pro 825
Thr	Leu	Ala	Pro	Pro 830	Gln	Pro	Pro	Leu	Pro 835	Glu	Thr	Ile	Glu	Arg 840
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Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile  
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Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln  
875 880 885

Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro  
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Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His  
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Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala  
920 925 930

Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala  
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Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu  
950 955 960

Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His  
965 970 975

Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly  
980 985 990

Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro  
995 1000 1005

Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys  
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1070 1075 1080

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cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600  
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<210> 63  
<211> 487  
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<213> Homo sapiens

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<222> 196, 386  
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Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val  
50 55 60  
Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro  
65 70 75  
Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser  
80 85 90  
Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg  
95 100 105  
Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe  
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Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val  
125 130 135  
Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp  
140 145 150  
Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His  
155 160 165  
Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala  
170 175 180  
Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val  
185 190 195  
Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser  
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Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys  
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Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met  
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Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val  
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Val Ile Phe Ser His Ser Ala Ala Arg	Ala Val Cys Asp Asn Leu	
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Leu Asn Val Pro Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly Gly	
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly	Val Leu Gln Cys Asn Leu	
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp	His Phe Asp His Ile Arg	
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp	
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Gly Thr Gly Arg Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr	
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu	
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg	
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val	
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser	
425	430	435
His Leu Val Pro Gln Asn Gly His Gln	Ala Thr His Leu Glu Val	
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala	
455	460	465
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 <223> Synthetic construct.

<400> 65  
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<210> 67  
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<400> 67  
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 tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300  
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<212> PRT  
<213> Homo sapiens

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Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
65 70 75  
Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
80 85 90  
Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
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Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
110 115 120  
Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
125 130 135  
Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
140 145 150  
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
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Met Leu Ser

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<212> DNA  
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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25				30	
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45

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 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
 65 70 75  
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
 80 85 90  
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
 95 100 105  
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
 110 115 120  
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu  
 125 130 135  
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg  
 140 145 150  
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu  
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 170 175 180  
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 185 190 195  
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln  
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 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu  
 215 220 225  
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 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val  
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<210> 71  
 <211> 1809  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250  
atatttttagt aattcatatg ttttagatta taggttttaa catacttgtg 300  
aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350  
ggatttgttc ttttatcccc cttttaaagt catccgtcct tggctcagga 400  
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tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500  
gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550  
ctcaagcccc caacatccca gtcctcagtc ctcagtcatc ttgacttcaa 600  
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agcaccagag ccaggcagtc actgttcctc ctccctggttt ggagtccttt 700  
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Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala  
245 250 255

Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser  
260 265 270

Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser  
275 280 285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln  
290 295 300

Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn  
305 310 315

Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr  
320 325 330

Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg  
335 340 345

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Leu Ile Arg

<210> 73  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 73  
aattcatggc aaatatattcc cttccc 26

<210> 74  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 74  
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<210> 75  
<211> 50



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cccttcagc ggctgggtccc gctttcctgg aatttggcct gggcgtatgc 1200  
agaggccgcc tccacacccc tccccaggg gcttgggtggc agcatagccc 1250  
ccacccctgc ggcttttgct cacgggtggc cctgcccacc cctggcacia 1300  
ccaaaatccc actgatgccc atcatgccct cagacccttc tgggctctgc 1350  
ccgctggggg cctgaagaca ttcctggagg aactcccat cagaacctgg 1400  
cagccccaaa actggggtca gcctcagggc aggagtccca ctccctccagg 1450  
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<210> 77  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 77  
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Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
35 40 45  
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
50 55 60  
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
65 70 75

Ala	Arg	Gly	Ala	Pro 80	Ala	Leu	Leu	Thr	Cys 85	Val	Asn	Arg	Gly	His 90
Val	Trp	Thr	Asp	Arg 95	His	Val	Glu	Glu	Ala 100	Gln	Gln	Val	Val	His 105
Trp	Asp	Arg	Gln	Pro 110	Pro	Gly	Val	Pro	His 115	Asp	Arg	Ala	Asp	Arg 120
Leu	Leu	Asp	Leu	Tyr 125	Ala	Ser	Gly	Glu	Arg 130	Arg	Ala	Tyr	Gly	Pro 135
Leu	Phe	Leu	Arg	Asp 140	Arg	Val	Ala	Val	Gly 145	Ala	Asp	Ala	Phe	Glu 150
Arg	Gly	Asp	Phe	Ser 155	Leu	Arg	Ile	Glu	Pro 160	Leu	Glu	Val	Ala	Asp 165
Glu	Gly	Thr	Tyr	Ser 170	Cys	His	Leu	His	His 175	His	Tyr	Cys	Gly	Leu 180
His	Glu	Arg	Arg	Val 185	Phe	His	Leu	Thr	Val 190	Ala	Glu	Pro	His	Ala 195
Glu	Pro	Pro	Pro	Arg 200	Gly	Ser	Pro	Gly	Asn 205	Gly	Ser	Ser	His	Ser 210
Gly	Ala	Pro	Gly	Pro 215	Asp	Pro	Thr	Leu	Ala 220	Arg	Gly	His	Asn	Val 225
Ile	Asn	Val	Ile	Val 230	Pro	Glu	Ser	Arg	Ala 235	His	Phe	Phe	Gln	Gln 240
Leu	Gly	Tyr	Val	Leu 245	Ala	Thr	Leu	Leu	Leu 250	Phe	Ile	Leu	Leu	Leu 255
Val	Thr	Val	Leu	Leu 260	Ala	Ala	Arg	Arg	Arg 265	Arg	Gly	Gly	Tyr	Glu 270
Tyr	Ser	Asp	Gln	Lys 275	Ser	Gly	Lys	Ser	Lys 280	Gly	Lys	Asp	Val	Asn 285
Leu	Ala	Glu	Phe	Ala 290	Val	Ala	Ala	Gly	Asp 295	Gln	Met	Leu	Tyr	Arg 300
Ser	Glu	Asp	Ile	Gln 305	Leu	Asp	Tyr	Lys	Asn 310	Asn	Ile	Leu	Lys	Glu 315
Arg	Ala	Glu	Leu	Ala 320	His	Ser	Pro	Leu	Pro 325	Ala	Lys	Tyr	Ile	Asp 330
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<210> 78
<211> 2243
<212> DNA
<213> Homo sapiens
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<400> 78

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<210> 79  
<211> 475  
<212> PRT  
<213> Homo sapiens

<400> 79  
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35 40 45  
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu  
50 55 60  
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys  
65 70 75  
Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr  
80 85 90  
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser  
95 100 105



									395						400						405
Thr	Val	Val	Phe	Gln	Ser	Asp	Val	Tyr	Pro	Ala	Leu	Leu	Ser	Ser							
				410					415					420							
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				425					430					435							
Tyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Thr	Gly							
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Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly	Ser							
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<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

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<210> 81
<211> 23
<212> DNA
<213> Homo sapiens
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<400> 81
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<220>  
<221> Artificial sequence  
<222> 1-49  
<223> Synthetic construct.

$$\begin{array}{ll} \langle 210 \rangle & 83 \\ \langle 211 \rangle & 1844 \end{array}$$

<212> DNA

<213> Homo sapiens

<400> 83

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<210> 84  
<211> 567  
<212> PRT  
<213> Homo sapiens

<400> 84  
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Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
35 40 45  
Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
50 55 60  
Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
65 70 75  
Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
80 85 90  
Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
95 100 105  
Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
110 115 120  
His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
125 130 135  
Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
140 145 150  
Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
155 160 165

Leu	Gly	Tyr	Ala	Leu 170	Arg	Pro	Gln	Glu	Lys 175	Gly	His	Ser	Pro	Glu 180
Asp	Ile	Tyr	Gln	Met 185	Ala	Leu	Asn	Gln	Ala 190	Leu	Lys	Asp	Leu	Lys 195
Ala	Leu	Gly	Cys	Arg 200	Lys	Ala	Met	Lys	Lys 205	Phe	Glu	Arg	His	Thr 210
Leu	Leu	Glu	Tyr	Leu 215	Leu	Gly	Glu	Gly	Asn 220	Leu	Ser	Arg	Pro	Ala 225
Val	Gln	Leu	Leu	Gly 230	Asp	Val	Met	Ser	Glu 235	Asp	Gly	Phe	Phe	Tyr 240
Leu	Ser	Phe	Ala	Glu 245	Ala	Leu	Arg	Ala	His 250	Ser	Cys	Leu	Ser	Asp 255
Arg	Leu	Gln	Tyr	Ser 260	Arg	Ile	Val	Gly	Gly 265	Trp	Asp	Leu	Leu	Pro 270
Arg	Ala	Leu	Leu	Ser 275	Ser	Leu	Ser	Gly	Leu 280	Val	Leu	Leu	Asn	Ala 285
Pro	Val	Val	Ala	Met 290	Thr	Gln	Gly	Pro	His 295	Asp	Val	His	Val	Gln 300
Ile	Glu	Thr	Ser	Pro 305	Pro	Ala	Arg	Asn	Leu 310	Lys	Val	Leu	Lys	Ala 315
Asp	Val	Val	Leu	Leu 320	Thr	Ala	Ser	Gly	Pro 325	Ala	Val	Lys	Arg	Ile 330
Thr	Phe	Ser	Pro	Pro 335	Leu	Pro	Arg	His	Met 340	Gln	Glu	Ala	Leu	Arg 345
Arg	Leu	His	Tyr	Val 350	Pro	Ala	Thr	Lys	Val 355	Phe	Leu	Ser	Phe	Arg 360
Arg	Pro	Phe	Trp	Arg 365	Glu	Glu	His	Ile	Glu 370	Gly	Gly	His	Ser	Asn 375
Thr	Asp	Arg	Pro	Ser 380	Arg	Met	Ile	Phe	Tyr 385	Pro	Pro	Pro	Arg	Glu 390
Gly	Ala	Leu	Leu	Leu 395	Ala	Ser	Tyr	Thr	Trp 400	Ser	Asp	Ala	Ala	Ala 405
Ala	Phe	Ala	Gly	Leu 410	Ser	Arg	Glu	Glu	Ala 415	Leu	Arg	Leu	Ala	Leu 420
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Asp	Gly	Thr	Gly	Val 440	Val	Lys	Arg	Trp	Ala 445	Glu	Asp	Gln	His	Ser 450
Gln	Gly	Gly	Phe	Val	Val	Gln	Pro	Pro	Ala	Leu	Trp	Gln	Thr	Glu

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Gly Gln Gly His Val His Gly Val Ala	Ser Ser Pro Ser His Asp	
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<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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				20					25				30	

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Phe	Asn	Phe	Leu	Phe 65	Ser	Pro	Leu	Pro	Thr 70	Pro	Ala	Leu	Ile	Cys 75
Ile	Leu	Thr	Phe	Gly 80	Ala	Ala	Ile	Phe	Leu 85	Trp	Leu	Ile	Thr	Arg 90
Pro	Gln	Pro	Val	Leu 95	Pro	Leu	Leu	Asp	Leu 100	Asn	Asn	Gln	Ser	Val 105
Gly	Ile	Glu	Gly	Gly 110	Ala	Arg	Lys	Gly	Val 115	Ser	Gln	Lys	Asn	Asn 120
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Phe	Asp	Asp	Asp	Leu 275	Lys	Gln	Arg	Gly	Glu 280	Lys	Ser	Gly	Ile	Glu 285
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Tyr	Ser	Cys	Gly	Ala 380	Arg	Val	Gly	Phe	Phe 385	Gln	Gly	Asp	Ile	Arg 390
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Ala	Val	Pro	Arg	Leu 410	Leu	Asn	Arg	Ile	Tyr 415	Asp	Lys	Val	Gln	Asn 420
Glu	Ala	Lys	Thr	Pro 425	Leu	Lys	Lys	Phe	Leu 430	Leu	Lys	Leu	Ala	Val 435
Ser	Ser	Lys	Phe	Lys 440	Glu	Leu	Gln	Lys	Gly 445	Ile	Ile	Arg	His	Asp 450
Ser	Phe	Trp	Asp	Lys 455	Leu	Ile	Phe	Ala	Lys 460	Ile	Gln	Asp	Ser	Leu 465
Gly	Gly	Arg	Val	Arg 470	Val	Ile	Val	Thr	Gly 475	Ala	Ala	Pro	Met	Ser 480
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Ala	Cys	Asn	Tyr	Val 530	Lys	Leu	Glu	Asp	Val 535	Ala	Asp	Met	Asn	Tyr 540
Phe	Thr	Val	Asn	Asn 545	Glu	Gly	Glu	Val	Cys 550	Ile	Lys	Gly	Thr	Asn 555
Val	Phe	Lys	Gly	Tyr 560	Leu	Lys	Asp	Pro	Glu 565	Lys	Thr	Gln	Glu	Ala 570
Leu	Asp	Ser	Asp	Gly 575	Trp	Leu	His	Thr	Gly 580	Asp	Ile	Gly	Arg	Trp 585
Leu	Pro	Asn	Gly	Thr 590	Leu	Lys	Ile	Ile	Asp 595	Arg	Lys	Lys	Asn	Ile 600
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<211> 660
<212> PRT
<213> Homo sapiens
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Phe	Leu	Leu	Val	Thr	Val	Ile	Val	Asn	Ile	Lys	Leu	Ile	Leu	Asp
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Thr	Arg	Arg	Ala	Ile	Ser	Glu	Ala	Asn	Glu	Asp	Pro	Glu	Pro	Glu
				65					70					75
Gln	Asp	Tyr	Asp	Glu	Ala	Leu	Gly	Arg	Leu	Glu	Pro	Pro	Arg	Arg
				80					85					90
Arg	Gly	Ser	Gly	Pro	Arg	Arg	Val	Leu	Asp	Val	Glu	Val	Tyr	Ser
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Ser	Arg	Ser	Lys	Val	Tyr	Val	Ala	Val	Asp	Gly	Thr	Thr	Val	Leu
				110					115					120
Glu	Asp	Glu	Ala	Arg	Glu	Gln	Gly	Arg	Gly	Ile	His	Val	Ile	Val
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Thr Tyr Ser Pro His Glu Asp Glu Ala	Met Val Leu Phe Leu Asn
155	160 165
Met Val Ala Pro Gly Arg Val Leu Ile	Cys Thr Val Lys Asp Glu
170	175 180
Gly Ser Phe His Leu Lys Asp Thr Ala	Lys Ala Leu Leu Arg Ser
185	190 195
Leu Gly Ser Gln Ala Gly Pro Ala Leu	Gly Trp Arg Asp Thr Trp
200	205 210
Ala Phe Val Gly Arg Lys Gly Gly Pro	Val Phe Gly Glu Lys His
215	220 225
Ser Lys Ser Pro Ala Leu Ser Ser Trp	Gly Asp Pro Val Leu Leu
230	235 240
Lys Thr Asp Val Pro Leu Ser Ser Ala	Glu Glu Ala Glu Cys His
245	250 255
Trp Ala Asp Thr Glu Leu Asn Arg Arg	Arg Arg Arg Phe Cys Ser
260	265 270
Lys Val Glu Gly Tyr Gly Ser Val Cys	Ser Cys Lys Asp Pro Thr
275	280 285
Pro Ile Glu Phe Ser Pro Asp Pro Leu	Pro Asp Asn Lys Val Leu
290	295 300
Asn Val Pro Val Ala Val Ile Ala Gly	Asn Arg Pro Asn Tyr Leu
305	310 315
Tyr Arg Met Leu Arg Ser Leu Leu Ser	Ala Gln Gly Val Ser Pro
320	325 330
Gln Met Ile Thr Val Phe Ile Asp Gly	Tyr Tyr Glu Glu Pro Met
335	340 345
Asp Val Val Ala Leu Phe Gly Leu Arg	Gly Ile Gln His Thr Pro
350	355 360
Ile Ser Ile Lys Asn Ala Arg Val Ser	Gln His Tyr Lys Ala Ser
365	370 375
Leu Thr Ala Thr Phe Asn Leu Phe Pro	Glu Ala Lys Phe Ala Val
380	385 390
Val Leu Glu Glu Asp Leu Asp Ile Ala	Val Asp Phe Phe Ser Phe
395	400 405
Leu Ser Gln Ser Ile His Leu Leu Glu	Glu Asp Asp Ser Leu Tyr
410	415 420
Cys Ile Ser Ala Trp Asn Asp Gln Gly	Tyr Glu His Thr Ala Glu



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Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys		
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg		
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
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Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
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Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
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Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
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575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
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<210> 94  
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<213> Homo sapiens

<400> 94

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<211> 307
<212> PRT
<213> Homo sapiens
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Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser
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Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser
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Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His
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Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu
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Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp
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Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu
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Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala
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Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val
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Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser
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Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His
				200					205					210
Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr
				215					220					225
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe	Ser Ala Gly Thr Phe Leu	
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro	Glu Val Gly Gly Ile Gly	
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser Arg	
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu Ile	
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 <213> Artificial

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 <222> 1-25  
 <223> Synthetic construct.

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<220>  
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 <223> Synthetic construct.

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<212> DNA

<213> Homo sapiens

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Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
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 <212> DNA  
 <213> Homo sapiens

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 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro  
 35 40 45  
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala  
 50 55 60  
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile  
 65 70 75  
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val  
 80 85 90  
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser  
 95 100 105  
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu  
 110 115 120  
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu  
 125 130 135  
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly  
 140 145 150  
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys  
 155 160 165  
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp  
 170 175 180  
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe  
 185 190 195  
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

200	205	210
Ile Leu Glu His Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp Asp	
215	220	225
Val Leu Ile Ala His Phe Leu Gly Val	Asp His Cys Gly His Lys	
230	235	240
His Gly Pro His His Pro Glu Met Ala	Lys Lys Leu Ser Gln Met	
245	250	255
Asp Gln Val Ile Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp Thr	
260	265	270
Leu Leu Val Val Ala Gly Asp His Gly	Met Thr Thr Asn Gly Asp	
275	280	285
His Gly Gly Asp Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe Leu	
290	295	300
Tyr Ser Pro Thr Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu Pro	
305	310	315
Glu Val Ile Pro Gln Val Ser Leu Val	Pro Thr Leu Ala Leu Leu	
320	325	330
Leu Gly Leu Pro Ile Pro Phe Gly Asn	Ile Gly Glu Val Met Ala	
335	340	345
Glu Leu Phe Ser Gly Gly Glu Asp Ser	Gln Pro His Ser Ser Ala	
350	355	360
Leu Ala Gln Ala Ser Ala Leu His Leu	Asn Ala Gln Gln Val Ser	
365	370	375
Arg Phe Leu His Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln Ala	
380	385	390
Lys Glu Leu His Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser Ala	
395	400	405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala Thr	
410	415	420
Leu Pro Thr Val Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly Ala	
425	430	435
Arg Ala Met Cys Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val Arg	
440	445	450
Met Ala Gly Gly Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile Cys	
455	460	465
Leu Leu Ala Ser Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe Cys	
470	475	480
Pro Leu Leu Leu Thr Pro Val Ala Trp	Gly Leu Val Gly Ala Ile	
485	490	495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu  
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Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe  
515 520 525

Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala  
530 535 540

Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Phe  
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Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala  
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Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val  
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Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu  
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Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg  
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His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu  
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Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr  
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Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met  
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Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala  
665 670 675

Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg  
680 685 690

Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg  
695 700 705

Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala  
710 715 720

Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu  
725 730 735

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu  
740 745 750

Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val  
755 760 765

Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu  
770 775 780

Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr



Arg Gln Leu Phe Leu Ala Gln Gln Arg  
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<210> 103  
<211> 1743  
<212> DNA  
<213> Homo sapiens

<400> 103  
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gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250



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 aaatgtttgc cagactgggt gcagaattta ttcagggtggg tgt 1743

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 <211> 442  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
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 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr  
 35 40 45  
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser  
 50 55 60  
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu  
 65 70 75  
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His  
 80 85 90  
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val  
 95 100 105  
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro  
 110 115 120  
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu  
 125 130 135  
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile  
 140 145 150  
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr  
 155 160 165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile  
170 175 180

Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys  
185 190 195

Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys  
200 205 210

Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val  
215 220 225

Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro  
230 235 240

Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu  
245 250 255

Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser  
260 265 270

Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys  
275 280 285

Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys  
290 295 300

Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser  
305 310 315

Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu  
320 325 330

Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp  
335 340 345

Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro  
350 355 360

Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr  
365 370 375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser  
380 385 390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly  
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro  
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly  
425 430 435

Leu Tyr Val Gln Met Glu Asn  
440

<210> 105

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<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
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<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

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<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp	20	25	30	
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg	35	40	45	
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly	50	55	60	
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys	65	70	75	
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala	80	85	90	
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile	95	100	105	
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala	110	115	120	
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly	125	130	135	
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro	140	145	150	
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val	155	160	165	
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val	170	175	180	
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His	185	190	195	
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg	200	205	210	
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg	215	220	225	
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly	230	235	240	
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val	245	250	255	

122

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tgtcaacgcc cggcacctgg acttggttcc cctcaagtct atccgagagt 400
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<210> 116  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 116  
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 20 25 30  
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
 35 40 45  
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
 50 55 60  
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
 65 70 75  
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
 80 85 90  
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
 95 100 105  
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
 110 115 120  
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
 125 130 135  
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
 140 145 150  
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
 155 160 165  
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
 170 175 180  
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn  
 185 190 195  
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe  
 200 205 210  
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val  
 215 220 225



Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

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Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	35	40	45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	50	55	60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	65	70	75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	80	85	90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	95	100	105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	110	115	120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	125	130	135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	140	145	150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	155	160	165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	170	175	180	
Gly	Asp	Asp	Cys	Phe	Gln	Val	Gly	Lys	Val	Ala	Tyr	Asp	Met	Gly	185	190	195	
Asp	Tyr	Tyr	His	Ala	Ile	Pro	Trp	Leu	Glu	Glu	Ala	Val	Ser	Leu	200	205	210	
Phe	Arg	Gly	Ser	Tyr	Gly	Glu	Trp	Lys	Thr	Glu	Asp	Glu	Ala	Ser	215	220	225	
Leu	Glu	Asp	Ala	Leu	Asp	His	Leu	Ala	Phe	Ala	Tyr	Phe	Arg	Ala	230	235	240	

Gly	Asn	Val	Ser	Cys 245	Ala	Leu	Ser	Leu	Ser 250	Arg	Glu	Phe	Leu	Leu 255
Tyr	Ser	Pro	Asp	Asn 260	Lys	Arg	Met	Ala	Arg 265	Asn	Val	Leu	Lys	Tyr 270
Glu	Arg	Leu	Leu	Ala 275	Glu	Ser	Pro	Asn	His 280	Val	Val	Ala	Glu	Ala 285
Val	Ile	Gln	Arg	Pro 290	Asn	Ile	Pro	His	Leu 295	Gln	Thr	Arg	Asp	Thr 300
Tyr	Glu	Gly	Leu	Cys 305	Gln	Thr	Leu	Gly	Ser 310	Gln	Pro	Thr	Leu	Tyr 315
Gln	Ile	Pro	Ser	Leu 320	Tyr	Cys	Ser	Tyr	Glu 325	Thr	Asn	Ser	Asn	Ala 330
Tyr	Leu	Leu	Leu	Gln 335	Pro	Ile	Arg	Lys	Glu 340	Val	Ile	His	Leu	Glu 345
Pro	Tyr	Ile	Ala	Leu 350	Tyr	His	Asp	Phe	Val 355	Ser	Asp	Ser	Glu	Ala 360
Gln	Lys	Ile	Arg	Glu 365	Leu	Ala	Glu	Pro	Trp 370	Leu	Gln	Arg	Ser	Val 375
Val	Ala	Ser	Gly	Glu 380	Lys	Gln	Leu	Gln	Val 385	Glu	Tyr	Arg	Ile	Ser 390
Lys	Ser	Ala	Trp	Leu 395	Lys	Asp	Thr	Val	Asp 400	Pro	Lys	Leu	Val	Thr 405
Leu	Asn	His	Arg	Ile 410	Ala	Ala	Leu	Thr	Gly 415	Leu	Asp	Val	Arg	Pro 420
Pro	Tyr	Ala	Glu	Tyr 425	Leu	Gln	Val	Val	Asn 430	Tyr	Gly	Ile	Gly	Gly 435
His	Tyr	Glu	Pro	His 440	Phe	Asp	His	Ala	Thr 445	Ser	Pro	Ser	Ser	Pro 450
Leu	Tyr	Arg	Met	Lys 455	Ser	Gly	Asn	Arg	Val 460	Ala	Thr	Phe	Met	Ile 465
Tyr	Leu	Ser	Ser	Val 470	Glu	Ala	Gly	Gly	Ala 475	Thr	Ala	Phe	Ile	Tyr 480
Ala	Asn	Leu	Ser	Val 485	Pro	Val	Val	Arg	Asn 490	Ala	Ala	Leu	Phe	Trp 495
Trp	Asn	Leu	His	Arg 500	Ser	Gly	Glu	Gly	Asp 505	Ser	Asp	Thr	Leu	His 510
Ala	Gly	Cys	Pro	Val 515	Leu	Val	Gly	Asp	Lys 520	Trp	Val	Ala	Asn	Lys 525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser



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 gggcgctcgc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450  
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500  
 ctcatcatgg agctcattgg tggcgtgggt gccttgacct tccggaacca 550  
 gaccattgac ttcctgaacg acaacattcg aagaggaatt gagaactact 600  
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
 aagtgtctgt gcggggagga ctaccgagat tggagcaaga atcagtacca 700  
 cgactgcagt gccctggac ccctggcctg tggggtgccc tacacctgct 750  
 gcatcaggaa cagcagagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
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 tgatgggctc ctggggcccc gtgccaagcc cagcgtggag gcggcaggca 1050  
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<210> 123  
 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 123  
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 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala  
 35 40 45  
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
 50 55 60  
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met  
 65 70 75  
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
 80 85 90  
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met  
 95 100 105  
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr  
 110 115 120  
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr  
 125 130 135  
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
 140 145 150  
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
 155 160 165  
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly  
 170 175 180  
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn  
 185 190 195  
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val  
 200 205 210  
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile  
 215 220 225  
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230		235		240
Ile Leu Leu Pro	Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu	Tyr		
	245	250	255		
Ile Thr Arg Val	Glu Asp Ile Ile Met	Glu His Ser Val Thr	Asp		
	260	265	270		
Gly Leu Leu Gly	Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala	Gly		
	275	280	285		
Thr Gly Cys Cys	Leu Cys Tyr Pro Asn				
	290				

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtgtt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
 cctgtctgtg ggcattctatg cagagggtga gcggcagaaa tataaaaccc 50

<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens





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gaaacccagc tctcctgtct cccagtgaag acttggatgg cagccatcag 1550  
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600  
cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128  
<211> 484  
<212> PRT  
<213> Homo sapiens

<400> 128  
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Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys  
35 40 45  
Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser  
50 55 60  
Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser  
65 70 75  
Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile  
80 85 90  
Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp  
95 100 105  
Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe  
110 115 120  
Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr  
125 130 135  
Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro  
140 145 150  
Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu  
155 160 165  
Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu  
170 175 180  
Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu  
185 190 195  
Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly  
200 205 210  
Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu  
215 220 225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys  
230 235 240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser  
245 250 255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu  
260 265 270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser  
275 280 285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu  
290 295 300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His  
305 310 315

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp  
320 325 330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr  
335 340 345

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu  
350 355 360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu  
365 370 375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr  
380 385 390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp  
395 400 405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp  
410 415 420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu  
425 430 435

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu  
440 445 450

Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys  
455 460 465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser  
470 475 480

Pro Val Ser Gln

<210> 129  
<211> 2213  
<212> DNA  
<213> Homo sapiens

<400> 129

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 aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150  
 ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200  
 gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250  
 ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
 agatcctggc aaactcctgg cgataactcca gtgcattcac caacaggata 350  
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 aaacatgaat tcagctccaa ctttcatcaa ctttctgca aaagggaaac 450  
 ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500  
 cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550  
 tagaccccca aattatgctg gtccccttat gttgggattg cttttggctg 600  
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 aataaaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700  
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 atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800  
 tttgtagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850  
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 tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300  
 aactactact ttgttttagt tagaacaag ctcaaaacta ctttagtta 1350  
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gaacaccatt	cttcagagca	cacgtctagc	cctcagcaag	acagttgttt	1600
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gcttgagtat	ggtgttaact	accttgtatt	tagaaagatt	tcagattcat	1750
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gcttagtgct	aaaatcagtg	taacttatac	atggcctaaa	atgtttctac	1850
aaattagagt	ttgtcactta	ttccatttgt	acctaagaga	aaaataggct	1900
cagttagaaa	aggactccct	ggccaggcgc	agtgacttac	gcctgtaatc	1950
tcagcacttt	gggaggccaa	ggcaggcaga	tcacgaggtc	aggagttcga	2000
gaccatcctg	gccaacatgg	tgaaaccccg	tctctactaa	aaatataaaa	2050
attagctggg	tgtggtggca	ggagcctgta	atcccagcta	cacaggaggc	2100
tgaggcacga	gaatcacttg	aactcaggag	atggagggtt	cagtgagccg	2150
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aaaaaaaaaa	aaa	2213			

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<210> 130
<211> 335
<212> PRT
<213> Homo sapiens
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<400> 130
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Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
20                25              30

Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
35                40              45

Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
50                55              60

Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
65                70              75

Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
80                85              90

Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
95                100             105

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Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp  
110 115 120

Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser  
125 130 135

Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg  
140 145 150

Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln  
155 160 165

Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val  
170 175 180

Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu  
185 190 195

Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met  
200 205 210

Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys  
215 220 225

Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg  
230 235 240

Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn  
245 250 255

Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His  
260 265 270

Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu  
275 280 285

Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys  
290 295 300

Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser  
305 310 315

Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr  
320 325 330

Ser Phe Leu Met Ser  
335

<210> 131  
<211> 2476  
<212> DNA  
<213> Homo sapiens

<400> 131  
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tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150  
cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200  
cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250  
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ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350  
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400  
ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450  
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aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550  
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ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050  
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ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagtg 1250  
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gtcaaaaacc tgcattccac ctggattctg agtgaattcc atggatgtaa 1350  
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cctattcgga tggatcatca atattgcctc aactctttga tctttctctg 1450  
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ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600  
ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650  
ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700  
aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagt 1750  
ttctagagat acatataaat atattacaag atcataatta tgtattttta 1800  
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<210> 132  
<211> 536  
<212> PRT  
<213> Homo sapiens

<400> 132  
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Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys  
20 25 30  
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg  
35 40 45  
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
50 55 60  
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
65 70 75



Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly	80	85	90
Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu	95	100	105
Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly	110	115	120
Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His	125	130	135
His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala	140	145	150
Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg	155	160	165
Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr	170	175	180
Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr	185	190	195
Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr	200	205	210
Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His	215	220	225
Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys	230	235	240
Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr	245	250	255
Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn			

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys		
380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser		
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg		
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile		
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr		
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln		
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val		
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

<210> 133  
<211> 1475  
<212> DNA  
<213> Homo sapiens

<400> 133  
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gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150  
ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200  
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catcaccag tgtgacatct atagaccct tctgggcctg cccgctgaca 350  
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 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600  
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650  
 ctggaatcat cctctgcttt tctgtctcat cccagagaaa tcgctccaac 700  
 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750  
 gcctgggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800  
 cagggtatgt gtgaagaacc agggggccaga gctgggggggt ggctgggtct 850  
 gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900  
 actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950  
 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000  
 attgccaaag atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050  
 gctcccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100  
 agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150  
 ccccaaacc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200  
 ccctctctct ggctgagggt ggctcttagc tcattgctgg ggatgggaag 1250  
 gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300  
 cctccaaaga aactgattgg ccttgaacc tccatcccac tcttgttatg 1350  
 actccacagt gtccagacta atttggtgcat gaactgaaat aaaaccatcc 1400  
 tacggtatcc agggaaacaga aagcaggatg caggatggga ggacaggaag 1450  
 gcagcctggg acatttaaaa aaata 1475

<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
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 1 5 10 15  
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 20 25 30  
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
 35 40 45  
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50	55	60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr	Leu Leu Gly Leu Pro Ala	
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met	Val Thr Ser Ser Ala Ile	
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val	Val Gly Met Arg Cys Thr	
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys	Asp Arg Val Ala Val Ala	
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly	Leu Leu Gly Phe Ile Pro	
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu	Arg Asp Phe Tyr Ser Pro	
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu	Ile Gly Glu Ala Leu Tyr	
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser	Leu Ile Ala Gly Ile Ile	
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg	Asn Arg Ser Asn Tyr Tyr	
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala	Thr Arg Ser Ser Pro Arg	
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser	Glu Phe Asn Ser Tyr Ser	
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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 aagtcacgcg tcccgcctggc tcagaacccat ggctgtgcca gccggcaccc 150  
 aggtgtggag acaagatcta caacccttg gagcagtgct gttacaatga 200  
 cgccatcgctg tccctgagcg agaccgcgcca atgtgggtccc ccctgcacct 250  
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcaciaaac 300  
 gattttgttg tgaagctgaa gggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400  
 acatagaaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600  
 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu  
 1 5 10 15  
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys  
 65 70 75  
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe  
 80 85 90  
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser  
 95 100 105  
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro  
 110 115

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
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 gtctttgcca ttttctgcat ctccaggctc ctctgtctac acggagcccc 100  
 agtggtcccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgtgcc cctggacctt catggtgaag ctgataaacc 300  
 agaactgcga ctcagcccgga acctcggtatg acaggctttg tcgcagtgtc 350  
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400  
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagt 450  
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550  
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600  
 ggactctgaa cctcctgat gaccctatg gccaacatca acccggcacc 650  
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700  
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750  
 tatgtacttt ataatgaaa a 771

<210> 138  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 138  
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys  
 1 5 10 15  
 Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met  
 20 25 30  
 Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp  
 35 40 45  
 Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val  
 50 55 60  
 Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg  
 65 70 75  
 Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu  
 80 85 90  
 Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu  
 95 100 105  
 Cys Arg Ser Val Ser  
 110

<210> 139  
 <211> 2044  
 <212> DNA  
 <213> Homo sapiens

<400> 139

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 gctcgcaactc agtcgcgagg ggttccccg cgccggccgc gtcccgcccg 100  
 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150  
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200  
 tctcttctcg gctgcgtccc taggtccggg ggcagccttc aaggtcgcca 250  
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 tgcaggctct tgggccctgt ggacaaagg cagcatgtga ccttctacaa 350  
 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400  
 ggcccatccg caacctcacg ttccaggacc ttacactgca ccatggaggc 450  
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500  
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550  
 ccctgctgga tagcggcctc tactgctgcc tgggtggtgga gatcaggcac 600  
 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650  
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700  
 atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750  
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 ggcagcctcc aaccgccgtg cccaggagct ggtgcggatg gacagcaaca 850  
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 ataccgagg ccaaagtcag gcaccccctg tcctatgtgg ccagcgga 950  
 gccttctgag tctgggcggc atctgcttcc ggagcccagc acccccctgt 1000  
 ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050  
 gactctccaa actttgaggt catctagccc agctggggga cagtgggctg 1100  
 ttgtggctgg gtctggggca ggtgcatttg agccagggt ggctctgtga 1150  
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 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250  
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 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400  
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tgggccaccc tcccaggcac cagacacagg gcacgggtgga gagacttctc 1500  
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 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800  
 gttgccccac cacttgagga tgggtgtgag ggaggtgggt ggggccttct 1850  
 gggaaggtga gtggagaggg gcacctgccc cccgcctcc ccatecccta 1900  
 ctccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950  
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 140  
 Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly  
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 20 25 30  
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro  
 35 40 45  
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val  
 50 55 60  
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser  
 65 70 75  
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg  
 80 85 90  
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln  
 95 100 105  
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu  
 110 115 120  
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn  
 125 130 135  
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu



Ile Arg His His	His Ser Glu His Arg	Val His Gly Ala Met	Glu
	155	160	165
Leu Gln Val Gln	Thr Gly Lys Asp Ala	Pro Ser Asn Cys Val	Val
	170	175	180
Tyr Pro Ser Ser	Ser Gln Asp Ser Glu	Asn Ile Thr Ala Ala	Ala
	185	190	195
Leu Ala Thr Gly	Ala Cys Ile Val Gly	Ile Leu Cys Leu Pro	Leu
	200	205	210
Ile Leu Leu Leu	Val Tyr Lys Gln Arg	Gln Ala Ala Ser Asn	Arg
	215	220	225
Arg Ala Gln Glu	Leu Val Arg Met Asp	Ser Asn Ile Gln Gly	Ile
	230	235	240
Glu Asn Pro Gly	Phe Glu Ala Ser Pro	Pro Ala Gln Gly Ile	Pro
	245	250	255
Glu Ala Lys Val	Arg His Pro Leu Ser	Tyr Val Ala Gln Arg	Gln
	260	265	270
Pro Ser Glu Ser	Gly Arg His Leu Leu	Ser Glu Pro Ser Thr	Pro
	275	280	285
Leu Ser Pro Pro	Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu	Asp
	290	295	300
Pro Val Pro Asp	Ser Pro Asn Phe Glu	Val Ile	
	305	310	

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 cttagacctc ctttctgccc ctcttttctt gccaccgct gcttcttggc 150  
 ctttctccga ccccgctcta gcagcagacc tcctgggggc tgtgggttga 200  
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250  
 ccgctcccg accagcggcc tgacctggg gaaaggatgg ttcccgaggt 300  
 gaggtcctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg 350  
 actccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400  
 agatactccc ccggcgagag ctggcaccoc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttggt 500  
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550  
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600  
ggccccacca aagtccctgcc agcacaacgg gaccatgtac caacacggag 650  
agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700  
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
ccccgaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800  
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850  
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900  
tgggagaaaag agaggcccg gacccccagc cccactggc ctcagcgccc 950  
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000  
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100  
tcggccccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150  
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200  
agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250  
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
ctcgtccaca catcgggtatc cccaagccca gacaacctgc gtcgctttgc 1350  
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400  
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450  
ccacacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500  
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550  
gaaggctact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600  
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700  
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142  
<211> 451  
<212> PRT  
<213> Homo sapiens  
<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala
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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp
				20					25					30
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser
				35					40					45
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg
				50					55					60
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His
				65					70					75
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln
				80					85					90
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg
				95					100					105
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His
				110					115					120
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro
				125					130					135
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys
				140					145					150
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro
				155					160					165
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu
				170					175					180
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg
				185					190					195
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly
				200					205					210
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe
				215					220					225
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val
				230					235					240
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly
				245					250					255
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg
				260					265					270
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly
				275					280					285
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys

290										295					300				
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro					
				305					310					315					
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg					
				320					325					330					
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser					
				335					340					345					
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala					
				350					355					360					
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu					
				365					370					375					
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His					
				380					385					390					
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala					
				395					400					405					
Arg	Leu	Pro	Glu	Arg	Gly	Thr	Ala	Leu	Pro	Thr	Ala	Arg	Trp	Pro					
				410					415					420					
Pro	Arg	Arg	Ser	Leu	Glu	Arg	Leu	Pro	Ser	Pro	Asp	Pro	Gly	Ala					
				425					430					435					
Glu	Gly	His	Gly	Gln	Ser	Arg	Gln	Ser	Asp	Gln	Asp	Ile	Thr	Lys					
				440					445					450					

Thr

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
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 cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccattggattc 100  
 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
 tgggctacgc gctcctcggt atcgtgacct cgaggagagc gcggaagcag 200  
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300  
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350  
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctc gtgggcgccg 400  
 gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500  
 gtgagctgcc gtccgggtgag cacgtttccc ccaaaccctg gactgactgc 550  
 ttttaagggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
 1 5 10 15  
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
 20 25 30  
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
 35 40 45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
 50 55 60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
 65 70 75  
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
 80 85 90  
 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 ttgaggggaa gaggctgact gtacgttcct tctaactctgg caccactctc 100  
 caggctgcca tggggcccag caccctctc ctcatcttgt tccttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttggtg gactacatgg 200  
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
 actgctggag gtggcagaga aggagcggga ggcaactcaga actgaggccg 350  
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450  
 tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500  
 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550  
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600  
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<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

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			20					25						30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
			35					40						45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
			50					55						60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
			65					70						75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
			80					85						90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
			95					100						105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
			110					115						120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
			125					130						135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
			140					145						150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
			155					160						165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
			170					175						180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
			185					190						195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
			200					205						210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
			215					220						225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
			230					235						240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
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<210> 148  
<211> 500  
<212> PRT  
<213> Homo sapiens

<400> 148  
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Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys  
35 40 45  
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe  
50 55 60  
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe  
65 70 75  
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp  
80 85 90  
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr  
95 100 105  
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser  
110 115 120  
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly  
125 130 135  
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile  
140 145 150  
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala  
155 160 165  
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg  
170 175 180  
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu  
185 190 195  
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His  
200 205 210  
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp  
215 220 225  
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<211> 24

<212> DNA  
<213> Artificial

<220>  
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<223> Synthetic construct.

<400> 149  
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<210> 150  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
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<223> Synthetic construct.

<400> 150  
ggaactgacc cagtgtgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-45  
<223> Synthetic construct.

<400> 151  
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<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
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aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150  
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200  
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cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300  
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 <211> 258  
 <212> PRT  
 <213> Homo sapiens

<400> 153  
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 35 40 45  
 Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala  
 50 55 60  
 Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala  
 65 70 75  
 Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro  
 80 85 90  
 Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr  
 95 100 105  
 Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala  
 110 115 120  
 Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro  
 125 130 135  
 Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val  
 140 145 150  
 Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro  
 155 160 165  
 Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

	170		175		180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys	Asn		
	185		190		195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln	Thr		
	200		205		210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His	Cys		
	215		220		225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly	Leu		
	230		235		240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile	Pro		
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Cys Asn Arg

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-24  
 <223> Synthetic construct.

<400> 154  
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<210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 155  
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<210> 156  
 <211> 38  
 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-38  
 <223> Synthetic construct.

<400> 156  
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<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
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<210> 158  
 <211> 163  
 <212> PRT  
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<400> 158  
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 35 40 45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
 50 55 60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
 65 70 75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
 80 85 90



1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu  
95 100 105  
Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile  
110 115 120  
Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu  
125 130 135  
Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu  
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<210> 159  
<211> 1665  
<212> DNA  
<213> Homo sapiens

<400> 159  
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gtaaactgct gacgatgcag agttccgtga cggatgcagga aggcctgtgt 150  
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aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300  
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400  
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
gtgagcaggg gacacccct atgatctcct ggataggac ctccgtgtcc 600  
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Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr  
35 40 45  
Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr  
50 55 60  
Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala  
65 70 75  
Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg  
80 85 90  
Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser  
95 100 105  
Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

				110					115					120
Met	Glu	Lys	Gly	Ser 125	Ile	Lys	Trp	Asn	Tyr 130	Lys	His	His	Arg	Leu 135
Ser	Val	Asn	Val	Thr 140	Ala	Leu	Thr	His	Arg 145	Pro	Asn	Ile	Leu	Ile 150
Pro	Gly	Thr	Leu	Glu 155	Ser	Gly	Cys	Pro	Gln 160	Asn	Leu	Thr	Cys	Ser 165
Val	Pro	Trp	Ala	Cys 170	Glu	Gln	Gly	Thr	Pro 175	Pro	Met	Ile	Ser	Trp 180
Ile	Gly	Thr	Ser	Val 185	Ser	Pro	Leu	Asp	Pro 190	Ser	Thr	Thr	Arg	Ser 195
Ser	Val	Leu	Thr	Leu 200	Ile	Pro	Gln	Pro	Gln 205	Asp	His	Gly	Thr	Ser 210
Leu	Thr	Cys	Gln	Val 215	Thr	Phe	Pro	Gly	Ala 220	Ser	Val	Thr	Thr	Asn 225
Lys	Thr	Val	His	Leu 230	Asn	Val	Ser	Tyr	Pro 235	Pro	Gln	Asn	Leu	Thr 240
Met	Thr	Val	Phe	Gln 245	Gly	Asp	Gly	Thr	Val 250	Ser	Thr	Val	Leu	Gly 255
Asn	Gly	Ser	Ser	Leu 260	Ser	Leu	Pro	Glu	Gly 265	Gln	Ser	Leu	Arg	Leu 270
Val	Cys	Ala	Val	Asp 275	Ala	Val	Asp	Ser	Asn 280	Pro	Pro	Ala	Arg	Leu 285
Ser	Leu	Ser	Trp	Arg 290	Gly	Leu	Thr	Leu	Cys 295	Pro	Ser	Gln	Pro	Ser 300
Asn	Pro	Gly	Val	Leu 305	Glu	Leu	Pro	Trp	Val 310	His	Leu	Arg	Asp	Ala 315
Ala	Glu	Phe	Thr	Cys 320	Arg	Ala	Gln	Asn	Pro 325	Leu	Gly	Ser	Gln	Gln 330
Val	Tyr	Leu	Asn	Val 335	Ser	Leu	Gln	Ser	Lys 340	Ala	Thr	Ser	Gly	Val 345
Thr	Gln	Gly	Val	Val 350	Gly	Gly	Ala	Gly	Ala 355	Thr	Ala	Leu	Val	Phe 360
Leu	Ser	Phe	Cys	Val 365	Ile	Phe	Val	Val	Val 370	Arg	Ser	Cys	Arg	Lys 375
Lys	Ser	Ala	Arg	Pro 380	Ala	Ala	Gly	Val	Gly 385	Asp	Thr	Gly	Ile	Glu 390
Asp	Ala	Asn	Ala	Val 395	Arg	Gly	Ser	Ala	Ser 400	Gln	Gly	Pro	Leu	Thr 405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala  
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 Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser  
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 Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg  
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